96 Incidence of nephrotoxicity associated with concomitant colistimethate and vancomycin use in cystic fibrosis patients

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Objectives: Acute renal failure is not a characteristic presentation in cystic fibrosis (CF). However, pulmonary exacerbation may require treatment with potentially nephrotoxic antibiotics. Nephrotoxicity occurs in 3–5% of CF patients on colistimethate [1], but the risk with concomitant vancomycin use is unknown. We compared the incidence of acute kidney injury (AKI) with colistimethate alone (C) or in combination with vancomycin (C+V).
Method: Retrospective review of CF patients admitted from August 2008 – August 2012 on intravenous colistimethate. Exclusion criteria: antibiotic therapy <72 hours, baseline ESRD and pregnancy. Outcomes evaluated: AKI defined by the RIFLE criteria [2], change in serum creatinine and length of stay (LOS).
Conclusion: Preliminary findings reveal that the incidence of AKI was significantly increased with C+V compared to C alone (15.4% vs. 0%, p = 0.047). Median LOS was also greater with C+V (12 vs. 8 days, p = 0.019). In both groups, median colistimethate daily dose was similar (4.6 vs. 4.7 mg/kg, p = 0.86). Increased LOS with C+V may be secondary to AKI management, or conversely may represent a cohort of patients with more severe disease.

	C (N = 28)	C+V (N = 26)	P value
Demographics			
Median age (IQR)	26 (22, 29)	25 (23.8, 27)	0.473
Median FEV1 % (IQR)	52 (33, 68)	45 (27.3, 53.8)	0.091
Outcomes			
AKI (%)	0 (0)	4 (15.4)	0.047
Median LOS (IQR)	8 (6.3, 11)	12 (7, 16.5)	0.019

Reference(s)

[1] Beringer P. The clinical use of colistin in patients with CF. *Curr Opin Pulmon Med* 2001, 7: 434–440.
[2] Bellomo R, et al. Acute renal failure—definition, outcome measures, animal models, fluid therapy and information technology needs. *Crit Care* 2004; 8: 204–12.

97 Antarctic bacteria as producers of antibiotic volatile compounds inhibiting cystic fibrosis pathogens

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Microorganisms from extreme environments, such as Antarctica, are interesting since they have adopted peculiar survival strategies e.g. the synthesis of unusual bioactive molecules inhibiting the growth of other bacteria. In this work 26 Antarctic bacterial strains affiliated to different genera were tested for their ability to produce new natural drugs active *versus* member of the *Burkholderia cepacia* complex (Bcc), relevant pathogens in Cystic Fibrosis (CF) patients. The experiments were performed adopting the cross-streaking method using as target a panel of 40 Bcc strains. Moreover we tested the influence of the growth media on the ability of these Antarctic bacteria to inhibit the growth of Bcc species. To this purpose cross-streak experiments were carried out using Petri dishes with a central septum. The tester strains were grown on three different media, MA, TYP and PCA whereas Bcc (target) strains were grown only on PCA medium. Data obtained clearly revealed that most of Antarctic bacteria completely inhibit the growth of all the Bcc strains, probably through the production of a combination of diffusible and volatile molecules. Furthermore the production of such molecules may vary depending on the medium the tester strains are grown in. Further experiments performed by the SPME-GC-MS technique, revealed the production of different compounds. Finally these data highlight the potentiality of Antarctic bacteria as novel sources of antibacterial substances. For this reason the genomes of these 26 Antarctic strains were sequenced and assembled and further analysis will be conducted in order to identify the gene sets involved in the production of the volatile compounds.

98 Searching for new antimicrobial targets in *Burkholderia* genus: *In silico* analysis of the RND superfamily

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The genus *Burkholderia* includes a variety of species, with opportunistic human pathogenic strains, whose increasing resistance to antibiotics has become a public health problem. A major role in multi-drug resistance could be played by multidrug efflux pumps belonging to the RND superfamily, an ubiquitous group of proteins that appears to be mainly involved in antibiotic resistance in Gram$^-$ bacteria.
Objectives and Methods: We performed a deep analysis of the distribution of representatives of all the 8 families belonging to this superfamily in 26 *Burkholderia* completely sequenced genomes, to evaluate their possible use as a target for novel antimicrobial drugs. A total of 417 putative RND proteins were identified. Through different *in silico* analyses, most of these sequences were characterized and a *core* of proteins conserved in all *Burkholderia* genomes was identified.
Conclusion: The whole body of data obtained on the presence and distribution of RND proteins in *Burkholderia* genus shed some light on both the physiological role(s) played by these proteins and their evolution in this genus; besides, the *core* of proteins identified might serve as a basis for experimental tests, already in progress, aimed at checking their possible use as novel targets in antimicrobial therapy against *Burkholderia* species.
Lastly, the analyses performed allowed to refine the genome annotation of the genomes analyzed.

99 Performance of MALDI-TOF mass spectrometry method for identification of bacteria commonly isolated from cystic fibrosis patients

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Introduction: The accurate identification of pathogenic organisms from the respiratory secretions of cystic fibrosis (CF) patients is important to infection management and epidemiology. Routine phenotypic methods may lead to misidentification of bacteria. The development of MALDI-TOF-MS devices has revolutionized the routine identification by introducing an easy, rapid, and low-cost technique. The objective was to identify common bacterial isolates from CF patients by MALDI-TOF-MS.
Methods: Fifty three patients were enrolled and 85 specimens cultured for isolation of bacteria. We tested 125 isolates by routine phenotypic test including Vitek II, and by MALDI-TOF (Bruker).
Results: A total 13 bacterial species were evaluated using MALDI-MS identified isolates to species level (98% score >2) of tested isolates with genus agreement in 100%. Isolates were *Staphylococcus aureus* (n = 50, 40%), *Pseudomonas aeruginosa* (n = 40, 32%), *Haemophilus influenzae* (n = 17, 13.6%), *Achromobacter xylosoxidans* (n = 6, 4.8%), *Streptococus pyogens* (n = 2, 1.6%), *Haemophilus parahaemolyticus* (n = 2, 1.6%), *Streptococus pneumonae* (n = 2, 1.6%), and (n = 1, <1%) for each *Moraxella catarrhalis*, *Chrysobacterium gleum*, *Enterococcus cloacae*, *Haemophilus para*influenzae, *Neisseria perflava*, and *Stenotrophomonas multophilia*.
Discrepant isolates were two isolates of *Achromobacter* sp. identified by MALDI-MS as *Achromobacter xylosoxidans* (score >2), and *Neiseria* sp. identified as *Neisseria perflava* (score >2).
Conclusion: We demonstrated complete genus, species agreement with MALDI-MS compared to routine phenotypic identification. MALDI-MS will decrease time to results to optimize early antimicrobial therapy in CF patients.